



1 GTCCTTCCACCATGCACTCGCTGGGCTTCTTCTCTGTGGCGTGTCTCTGTCTGCTCGCCGCTG 60  
-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+  
CAGGAAGGTGTACGTGAGCGACCCGAAGAAGAGACACCCGACCAAGAGACGAGCGCGGAC  
M H S L G F F S V A C S L L A A A -  
CGCTGCTCCCGGGTCTCGCGAGGCGCCCGCCCGCCCGCCCTTCGAGTCCGGACTCG 120  
-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+  
GCGACGAGGGCCAGGAGCGCTCCGGCGGGCGGGCGGGGGAAGCTCAGGCCTGAGC  
L L P G P R E A P A A A A A F E S G L D -  
ACCTCTCGGACGCGGAGCCCGACGCGGGCGAGCCACGGCTTATGCAAGCAAGATCTGG 180  
-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+  
TGGAGAGCCTGCGCCCTCGGGCTGCGCCCGCTCCGGTGCCGAATACGTTCTCTAGACC  
L S D A E P D A G E A T A Y A S K D L E -  
AGGAGCAGTTACGGTCTGTGTCCAGTGTAGATGAACCTCATGACTGTACTCTACCCAGAAT 240  
-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+  
TCCCTCGTCAATGCCAGACACAGGTCACATCTACTTGAGTACTGACATGAGATGGGTCTTA  
E Q L R S V S S V D E L M T V L Y P E Y -  
ATTGGAAAATGTACAAGTGTACGCTAAGGAAGGAGGCTGGCAACATAACAGAGAACAGG 300  
-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+  
TAACCTTTTACATGTTACAGTCGATTCCTTTCCCTCCGACCGTTGTATTGTCTCTGTGCC  
W K M Y K C Q L R K G G W Q H N R E Q A -  
CCAACCTCAACTCAAGGACAGAAGAGACTATAAAATTGTGCTGCAGCACATTATAATACAG

FIG. 1A

301 -----+-----+-----+-----+-----+-----+-----+ 360  
GGTGGAGTTGAGTTCCTGTCTTCTCTGATATTTAAACGACGTCGTGTAATATATGTC  
N L N S R T E E T I K F A A A H Y N T E -  
361 AGATCTGAAAAGTATTGATAATGAGTGGAGAAAGACTCAATGCATGCCACGGGAGGTGT  
-----+-----+-----+-----+-----+-----+-----+ 420  
TCTAGAACTTTTCATAACTATTACTCACCTCTTTCTGAGTTACGTACGGTGCCCTCCACA  
I L K S I D N E W R K T Q C M P R E V C -  
421 GTATAGATGTGGGAAGGAGTTTGGAGTCGCGACAAACACCTTCTTTAAACCTCCATGTG  
-----+-----+-----+-----+-----+-----+-----+ 480  
CATATCTACACCCCTTCCTCAAAACCTCAGCGCTGTTGTGGAAGAAATTTGGAGGTACAC  
I D V G K E F G V A T N T F F K P P C V -  
481 TGTCCGCTACAGATGTGGGGTGTGCTGCAATAGTAGGGGCTGCAGTGCATGAACACCA  
-----+-----+-----+-----+-----+-----+-----+ 540  
ACAGGCAGATGTCTACACCCCCCAACGACGTTATCACTCCCCGACGTCACGTACTTGTTGGT  
S V Y R C G C C C N S E G L Q C M N T S -  
541 GCACGAGCTACCTCAGCAAGACGTTATTGAAATTACAGTGCCTCTCTCAAGGCCCA  
-----+-----+-----+-----+-----+-----+-----+ 600  
CGTGCTCGATGGAGTCGTTCTGCAATAAACTTTAATGTCACGGAGAGAGAGTCCGGGT  
T S Y L S K T L F E I T V P L S Q G P K -  
601 AACCAGTAACAATCAGTTTGGCCAATCACACTTCCTGCCGATGCATGCTCTAAACTGGATG  
-----+-----+-----+-----+-----+-----+-----+ 660  
TTGGTCATTTAGTCAAAACGGTTAGTGTGAAGGACGGCTACGTACAGATTGACCTAC  
P V T I S F A N H T S C R C M S K L D V -

FIG. 1B

TTTACAGACAAAGTTCAATTCATATATAGACGTTCCCTGCCAGCAACACTACCACAGTGTC 720  
-----+-----+-----+-----+-----+-----+-----+  
AAATGTCTCTGTTCAAGTAAGGTAATAATCTGCAAGGACGGTCGTTGTGATGGTGTCAACAG  
Y R Q V H S I I R R S L P A T L P Q C Q -  
AGGACGGAACAAGACCTGCCCCACCAATTACATGTGGAATAATCACATCTGCAGATGCC 780  
-----+-----+-----+-----+-----+-----+-----+  
TCCGTCGCTTGTTCTGGACGGGGTGGTTAAATGTACACCTTATAGTGTAGACGTCCTACGG  
A A N K T C P T N Y M W N N H I C R C L -  
TGGCTCAGGAAGATTTTATGTTTCCCTCGGATGCTGGAGATGACTCAACAGATGGATGCC 840  
-----+-----+-----+-----+-----+-----+-----+  
ACCGAGTCCCTTCTAAATAACAAAGGAGCCCTACGACCTCTACTGAGTTGTCTACCTAAGG  
A Q E D F M F S S D A G D S T D G F H -  
ATGACATCTGTGGACCAACAAGAGCTGGATGAAGAGACCTGTCAGTGTCTGCAGAG 900  
-----+-----+-----+-----+-----+-----+-----+  
TACTGTAGACACCTGGTTGTTCCCTCGACCTACTTCTCTGGACAGTCACACAGACGTCCTC  
D I C G P N K E L D E E T C Q C V C R A -  
CGGGGCTTCGGCCTGCCAGCTGTGGACCCCAAGAACTAGACAGAACTCATGCCAGT 960  
-----+-----+-----+-----+-----+-----+-----+  
GCCCCGAAGCCGGACGTCGACACCTGGGGTGTCTTCTTGATCTGTCTTTGAGTACGGTCA  
G L R P A S C G P H K E L D R N S C Q C -  
GTGTCTGTAAACAACACTCTTCCCCAGCCAATGTGGGGCCAACCGAGAAATTGATGAAA 1020  
-----+-----+-----+-----+-----+-----+-----+  
CACAGACATTTTGTGTTGAGAAGGGGTCGGTTACACCCCGGTTGGCTCTTAAACTACTTT

FIG. 1C

V C K N K L F P S Q C G A N R E F D E N -  
ACACATGCCAGTGTGTATGTAAAGAACCTGCCCCAGAAATCAACCCCTAAATCCTGGAA 1080  
-----+-----+-----+-----+-----+-----+-----+  
TGTGTACGGTCACACATACATTTCTTGGACGGGCTTTAGTTGGGGATTTAGGACCTT  
T C Q C V C K R T C P R N Q P L N P G K -  
AATGTGCCTGTGAATGTACAGAAAGTCCACAGAAATGCTTGTAAAGGAAAGAGTTCC 1140  
-----+-----+-----+-----+-----+-----+-----+  
TTACACGGACACTTACATGTCTTTCAGGTGTCTTTACGAACAATTTTCCTTCTCAAGG  
C A C E C T E S P Q K C L L K G K K F H -  
ACCACCAACATGCAGCTGTTACAGACGGCCATGTACGAACCGCCAGAGGCTTGTGAGC 1200  
-----+-----+-----+-----+-----+-----+-----+  
TGGTGGTTTGTACGTCGACAAATGTCTGCCGGTACATGCTTGGCGGTCTCCGAACACTCG  
H Q T C S C Y R R P C T N R Q K A C E P -  
CAGGATTTTCATATAGTGAAGAGTGTGTCGTTGTGTCCTTTCATATTTGGCAAGACCAC 1260  
-----+-----+-----+-----+-----+-----+-----+  
GTCCTAAAGTATATCACTTCTTTCACACAGCAACACAGGGAAGTATAACCGTTTCTGGTG  
G F S Y S E E V C C R C V P S Y W Q R P Q -  
AAATGAGCTAAGATTGTACTGTTTCCAGTTCATCGATTTTCTATTATGGAATACTGTGT

FIG. 1D

1261 -----+-----+-----+-----+-----+-----+-----+ 1320  
TTTACTCGATTCTAACATGACAAAAGGTCAAGTAGCTAAAAGATAATACCTTTTGACACA  
M S \*  
TGCCACAGTAGAACTGTCTGTGAACAGAGAGACCCCTTGTTGGTCCATGCTAACAAAGACA 1380  
1321 -----+-----+-----+-----+-----+-----+-----+  
ACGGTGTCACTTTGACAGACACTTGTCTCTCTCTGGGAACACCCAGGTACGATGTGTTCTGT  
AAAGTCTGTCTTTCCCTGAACCAATGTGGATAAATTTACAGAAATGGACTGGAGCTCATCTG 1440  
1381 -----+-----+-----+-----+-----+-----+-----+  
TTTCAGACAGAAAGGACTTGGTACACCTATTGAAATGTCTTTACCTGACCTCGAGTAGAC  
CAAAAGGCCCTCTTGTAAGAAGCTGTTTCTGCCCAATGACCAACAGCCAAAGATTTTCCCTC 1500  
1441 -----+-----+-----+-----+-----+-----+-----+  
GTTTTCGGGAGAACATTTCTGACCAAAAGACGGTTACTGTTTGTCTGCTCTCTAAAGGAG  
TTGTGATTTCTTTAAAGAATGACTATATAATTTATTTCCACTAAAAATATGTTTCTGTC 1560  
1501 -----+-----+-----+-----+-----+-----+-----+  
AACACTAAAGAAATTTCTTACTGATATATAATTAATAAAGGTGATTTTATATAACAAGACG  
ATTCATTTTATAGCAACAACAATTGGTAAAACTCACTGTGATCAATATTTTATATCAT 1620  
1561 -----+-----+-----+-----+-----+-----+-----+  
TAAGTAAATAATATCGTTGTTGTTAACCATTTTGAGTGACACTAGTTATAAAAAATATAGTA  
GCAAAATATGTTTAAATAAATAATGAAAAATTGTATTTATAAAAAAAATAAAAAA 1674  
1621 -----+-----+-----+-----+-----+-----+-----+  
CGTTTATACAAAATTTTATTTTACTTTTAAACATAAATAATTTTATTTTATTTT

FIG.1E

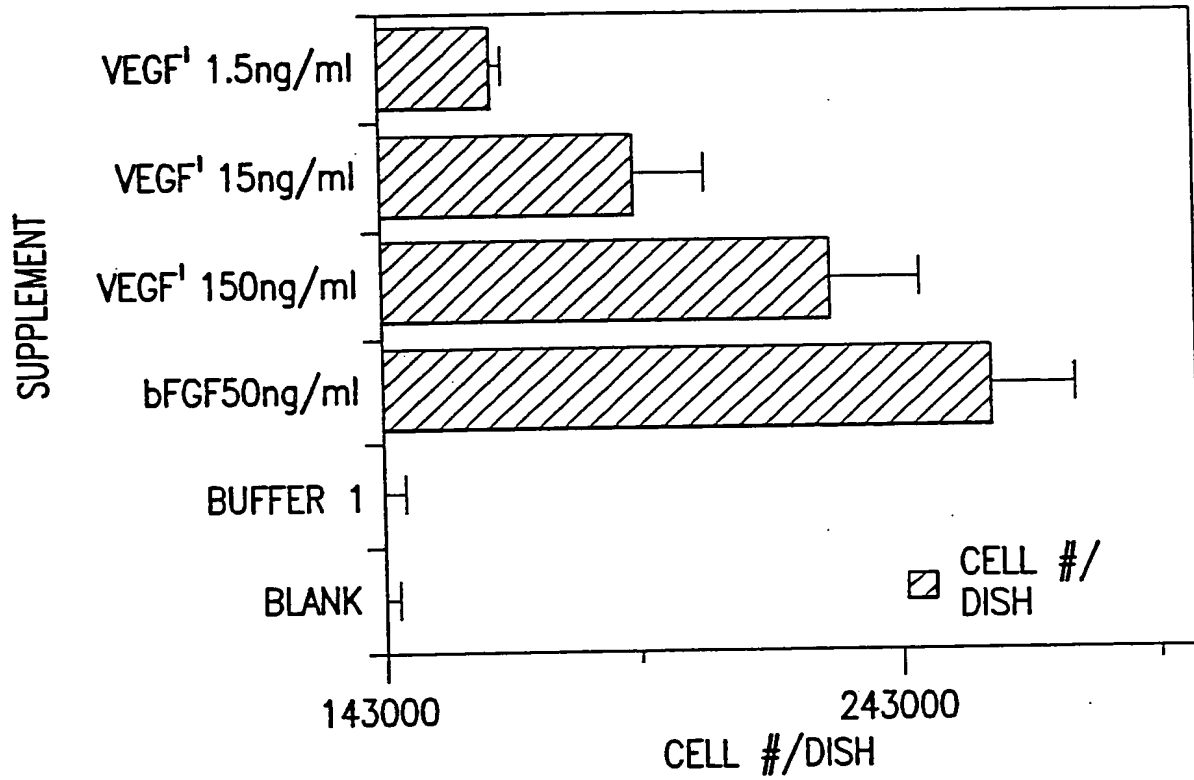


FIG.12

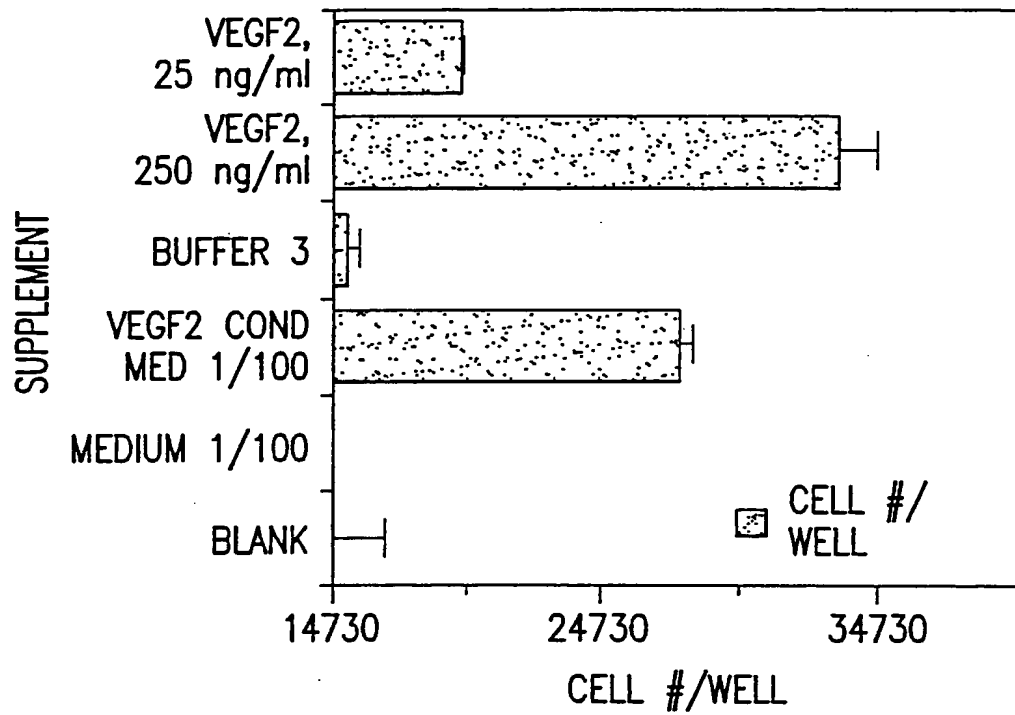


FIG.13